

SEQUENCE LISTING

5

(1) GENERAL INFORMATION:

(i) APPLICANT: Sato, Takaaki

10 (ii) TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING
EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES
THEREOF

(iii) NUMBER OF SEQUENCES: 37

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
20 (D) STATE: New York
(E) COUNTRY: U.S.A
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

25

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

30 (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

35 (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White, John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 0575/51902-A-PCT

40 (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525

45 (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3479 base pairs
(B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 458..3211

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TOPSECRET-031601

| | | | | | | | |
|----|---|------------|------------|------------|-------------------------|------------|------|
| | CCTGATCGTT | GGTAGTGGCA | TGGAGGACGG | GGCTGGCATT | TCAGACTGCC | AGCTGTTTTT | 60 |
| | ACCAGCCGCT | GCATCACTTG | AATAGAAGCT | ATGCATATTG | GCTGGCCGAC | AAAGCCAAGG | 120 |
| | 5GACAAAAGCT | ATGGCCGTTA | AAATGGTCCC | TCTGAGTCCA | GGGCTCTTTC | CCTGGCTTTT | 180 |
| | AGCACCATGG | ATCTCTTCCT | TTTCATCCCA | TCAGCAATGT | GGTACCTTCT | TCTACTTGAT | 240 |
| | GATGACAGCT | GATACTTCAG | ATTTGCCTGA | CTAAGGTTAG | AAACCTGAAT | CGCTGTGAGG | 300 |
| 10 | AAGATGAAAT | TTCCATTTTA | CTTGGTGCCT | TGTGCAGGGA | GCACACTGAT | CCTTCCAGAA | 360 |
| | ACTTGTGTGT | GAAAAGAGGT | TGCGTTTTGT | CAGACAGACT | CATGGTTATG | GCGAGCGATC | 420 |
| 15 | CGACGTGATC | AGAGTGGGCA | AGAGGCACAG | CGAACTC | ATG ACA GGC TAT ACC ATG | | 475 |
| | | | | | Met Thr Gly Tyr Thr Met | | |
| | | | | | 1 | 5 | |
| | TTG CGG AAT GGG GGA GTG GGG AAC GGT GGT CAG ACC TGT ATG CTG CGC | | | | | | 523 |
| 20 | Leu Arg Asn Gly Gly Val Gly Asn Gly Gly Gln Thr Cys Met Leu Arg | | | | | | |
| | | 10 | | 15 | | 20 | |
| | TGG TCC AAT CGC ATC CGG CTG ACA TGG CTG AGT TTC ACG CTG TTC ATC | | | | | | 571 |
| 25 | Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser Phe Thr Leu Phe Ile | | | | | | |
| | | 25 | | 30 | | 35 | |
| | ATC CTC GTC TTC TTC CCC CTC ATT GCT CAC TAT TAC CTC ACC ACT CTG | | | | | | 619 |
| 30 | Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr Tyr Leu Thr Thr Leu | | | | | | |
| | | 40 | | 45 | | 50 | |
| | GAC GAG GCA GAC GAG GCT GGC AAG CGC ATC TTC GGC CCT CGG GCT GGC | | | | | | 667 |
| | Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe Gly Pro Arg Ala Gly | | | | | | |
| | | 55 | | 60 | | 65 | 70 |
| 35 | AGT GAG CTC TGT GAG GTA AAG CAT GTC CTT GAT CTC TGT CGG ATT CGT | | | | | | 715 |
| | Ser Glu Leu Cys Glu Val Lys His Val Leu Asp Leu Cys Arg Ile Arg | | | | | | |
| | | | 75 | | | 80 | 85 |
| | GAG TCT GTG AGC GAA GAG CTT CTA CAG CTC GAA GCC AAG CGG CAG GAG | | | | | | 763 |
| 40 | Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu Ala Lys Arg Gln Glu | | | | | | |
| | | | 90 | | | 95 | 100 |
| | CTG AAC AGC GAG ATT GCC AAG CTG AAC CTC AAG ATT GAA GCC TGT AAG | | | | | | 811 |
| 45 | Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu Lys Ile Glu Ala Cys Lys | | | | | | |
| | | | 105 | | | 110 | 115 |
| | AAG AGC ATA GAG AAT GCC AAG CAG GAC CTG CTG CAG CTC AAG AAT GTC | | | | | | 859 |
| 50 | Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu Leu Gln Leu Lys Asn Val | | | | | | |
| | | | 120 | | | 125 | 130 |
| | ATT AGC CAG ACA GAG CAC TCC TAC AAG GAG CTG ATG GCC CAG AAC CAG | | | | | | 907 |
| | Ile Ser Gln Thr Glu His Ser Tyr Lys Glu Leu Met Ala Gln Asn Gln | | | | | | |
| | | | 135 | | | 140 | 145 |
| | CCC AAA CTG TCC CTG CCC ATC CGA CTG CTC CCT GAG AAG GAC GAT GCC | | | | | | 955 |
| 55 | Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu Pro Glu Lys Asp Asp Ala | | | | | | |
| | | | 155 | | | 160 | 165 |
| | GGC CTT CCA CCC CCC AAG GTC ACT CGG GGT TGC CGC CTT CAC AAC TGC | | | | | | 1003 |
| 60 | Gly Leu Pro Pro Pro Lys Val Thr Arg Gly Cys Arg Leu His Asn Cys | | | | | | |
| | | | 170 | | | 175 | 180 |
| | TTT GAT TAC TCT CGT TGT CCT CTG ACG TCT GGC TTT CCC GTC TAC GTC | | | | | | 1051 |

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| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | Phe | Asp | Tyr | Ser | Arg | Cys | Pro | Leu | Thr | Ser | Gly | Phe | Pro | Val | Tyr | Val | |
| | | 185 | | | | | | 190 | | | | | 195 | | | | |
| | TAT | GAC | AGT | GAC | CAG | TTT | GCC | TTT | GGG | AGC | TAC | CTG | GAC | CCT | TTG | GTC | 1099 |
| 5 | Tyr | Asp | Ser | Asp | Gln | Phe | Ala | Phe | Gly | Ser | Tyr | Leu | Asp | Pro | Leu | Val | |
| | | 200 | | | | | 205 | | | | | 210 | | | | | |
| | AAG | CAG | GCT | TTT | CAG | GCT | ACA | GTG | AGA | GCC | AAC | GTT | TAT | GTT | ACA | GAA | 1147 |
| 10 | Lys | Gln | Ala | Phe | Gln | Ala | Thr | Val | Arg | Ala | Asn | Val | Tyr | Val | Thr | Glu | |
| 215 | | | | | | 220 | | | | | 225 | | | | | 230 | |
| | AAT | GCG | GCC | ATC | GCC | TGC | CTG | TAT | GTG | GTG | TTA | GTG | GGA | GAA | ATG | CAA | 1195 |
| | Asn | Ala | Ala | Ile | Ala | Cys | Leu | Tyr | Val | Val | Leu | Val | Gly | Glu | Met | Gln | |
| | | | | | 235 | | | | | 240 | | | | | 245 | | |
| 15 | GAG | CCC | ACT | GTG | CTG | CGG | CCT | GCC | GAC | CTT | GAA | AAG | CAG | CTG | TTT | TCT | 1243 |
| | Glu | Pro | Thr | Val | Leu | Arg | Pro | Ala | Asp | Leu | Glu | Lys | Gln | Leu | Phe | Ser | |
| | | | | 250 | | | | | 255 | | | | | 260 | | | |
| 20 | CTG | CCA | CAC | TGG | AGG | ACA | GAT | GGG | CAC | AAC | CAC | GTC | ATT | ATC | AAC | CTG | 1291 |
| | Leu | Pro | His | Trp | Arg | Thr | Asp | Gly | His | Asn | His | Val | Ile | Ile | Asn | Leu | |
| | | | | 265 | | | | 270 | | | | | 275 | | | | |
| | TCC | CGG | AAG | TCA | GAC | ACA | CAG | AAT | CTA | CTG | TAC | AAC | GTC | AGT | ACA | GGC | 1339 |
| 25 | Ser | Arg | Lys | Ser | Asp | Thr | Gln | Asn | Leu | Leu | Tyr | Asn | Val | Ser | Thr | Gly | |
| | | 280 | | | | | 285 | | | | | 290 | | | | | |
| | CGC | CAT | GTG | GCC | CAG | TCC | ACC | CTC | TAT | GCT | GCC | CAG | TAC | AGA | GCT | GGC | 1387 |
| 30 | Arg | His | Val | Ala | Gln | Ser | Thr | Leu | Tyr | Ala | Ala | Gln | Tyr | Arg | Ala | Gly | |
| 295 | | | | | | 300 | | | | | 305 | | | | | 310 | |
| | TTT | GAC | CTG | GTC | GTG | TCA | CCC | CTT | GTC | CAT | GCT | ATG | TCT | GAA | CCC | AAC | 1435 |
| | Phe | Asp | Leu | Val | Val | Ser | Pro | Leu | Val | His | Ala | Met | Ser | Glu | Pro | Asn | |
| | | | | | 315 | | | | | 320 | | | | | 325 | | |
| 35 | TTC | ATG | GAA | ATC | CCA | CCG | CAG | GTG | CCA | GTT | AAG | CGG | AAA | TAT | CTC | TTC | 1483 |
| | Phe | Met | Glu | Ile | Pro | Pro | Gln | Val | Pro | Val | Lys | Arg | Lys | Tyr | Leu | Phe | |
| | | | | 330 | | | | | 335 | | | | | 340 | | | |
| 40 | ACT | TTC | CAG | GGC | GAG | AAG | ATC | GAG | TCT | CTG | AGA | TCT | AGC | CTT | CAG | GAG | 1531 |
| | Thr | Phe | Gln | Gly | Glu | Lys | Ile | Glu | Ser | Leu | Arg | Ser | Ser | Leu | Gln | Glu | |
| | | | | 345 | | | | 350 | | | | | 355 | | | | |
| | GCC | CGT | TCC | TTC | GAG | GAA | GAG | ATG | GAG | GGC | GAC | CCT | CCG | GCC | GAC | TAT | 1579 |
| 45 | Ala | Arg | Ser | Phe | Glu | Glu | Glu | Met | Glu | Gly | Asp | Pro | Pro | Ala | Asp | Tyr | |
| | | 360 | | | | | 365 | | | | | 370 | | | | | |
| | GAC | GAT | CGC | ATC | ATT | GCC | ACC | CTA | AAG | GCT | GTA | CAG | GAC | AGC | AAG | CTG | 1627 |
| 50 | Asp | Asp | Arg | Ile | Ile | Ala | Thr | Leu | Lys | Ala | Val | Gln | Asp | Ser | Lys | Leu | |
| 375 | | | | | | 380 | | | | | 385 | | | | | 390 | |
| | GAT | CAG | GTG | CTG | GTA | GAA | TTC | ACT | TGC | AAA | AAC | CAG | CCG | AAG | CCT | AGC | 1675 |
| | Asp | Gln | Val | Leu | Val | Glu | Phe | Thr | Cys | Lys | Asn | Gln | Pro | Lys | Pro | Ser | |
| | | | | | 395 | | | | | 400 | | | | | 405 | | |
| 55 | CTG | CCG | ACT | GAG | TGG | GCA | CTG | TGT | GGG | GAG | CGG | GAA | GAC | CGC | CTG | GAG | 1723 |
| | Leu | Pro | Thr | Glu | Trp | Ala | Leu | Cys | Gly | Glu | Arg | Glu | Asp | Arg | Leu | Glu | |
| | | | | 410 | | | | | 415 | | | | | 420 | | | |
| 60 | TTA | CTG | AAG | CTC | TCC | ACC | TTC | GCC | CTC | ATC | ATC | ACT | CCC | GGG | GAC | CCG | 1771 |
| | Leu | Leu | Lys | Leu | Ser | Thr | Phe | Ala | Leu | Ile | Ile | Thr | Pro | Gly | Asp | Pro | |
| | | | 425 | | | | | 430 | | | | | 435 | | | | |

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|-------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| CGC | CTG | CTC | ATT | TCA | TCT | GGG | TGT | GCC | ACG | CGG | CTC | TTC | GAG | GCC | CTG | 1819 |
| Arg | Leu | Leu | Ile | Ser | Ser | Gly | Cys | Ala | Thr | Arg | Leu | Phe | Glu | Ala | Leu | |
| 440 | | | | | | 445 | | | | | 450 | | | | | |
| 5GAG | GTG | GGG | GCC | GTG | CCG | GTG | GTG | CTC | GGG | GAG | CAG | GTG | CAG | CTC | CCG | 1867 |
| Glu | Val | Gly | Ala | Val | Pro | Val | Val | Leu | Gly | Glu | Gln | Val | Gln | Leu | Pro | |
| 455 | | | | | 460 | | | | | 465 | | | | | 470 | |
| TAC | CAC | GAC | ATG | CTG | CAG | TGG | AAC | GAG | GCC | GCC | CTG | GTG | GTG | CCC | AAG | 1915 |
| 10Tyr | His | Asp | Met | Leu | Gln | Trp | Asn | Glu | Ala | Ala | Leu | Val | Val | Pro | Lys | |
| | | | | 475 | | | | | 480 | | | | | 485 | | |
| CCT | CGC | GTC | ACA | GAG | GTC | CAC | TTC | CTG | TTA | CGA | AGT | CTT | TCA | GAC | AGT | 1963 |
| Pro | Arg | Val | Thr | Glu | Val | His | Phe | Leu | Leu | Arg | Ser | Leu | Ser | Asp | Ser | |
| 15 | | | 490 | | | | | 495 | | | | | 500 | | | |
| GAT | CTG | TTG | GCC | ATG | AGG | CGG | CAA | GGC | CGC | TTT | CTC | TGG | GAG | ACC | TAC | 2011 |
| Asp | Leu | Leu | Ala | Met | Arg | Arg | Gln | Gly | Arg | Phe | Leu | Trp | Glu | Thr | Tyr | |
| | | 505 | | | | | 510 | | | | | 515 | | | | |
| 20 | | | | | | | | | | | | | | | | |
| TTC | TCC | ACC | GCA | GAC | AGT | ATT | TTT | AAT | ACC | GTG | CTG | GCC | ATG | ATT | AGG | 2059 |
| Phe | Ser | Thr | Ala | Asp | Ser | Ile | Phe | Asn | Thr | Val | Leu | Ala | Met | Ile | Arg | |
| | 520 | | | | | 525 | | | | | 530 | | | | | |
| 25ACT | CGA | ATT | CAG | ATC | CCA | GCT | GCT | CCC | ATC | CGG | GAA | GAG | GTA | GCG | GCT | 2107 |
| Thr | Arg | Ile | Gln | Ile | Pro | Ala | Ala | Pro | Ile | Arg | Glu | Glu | Val | Ala | Ala | |
| 535 | | | | | 540 | | | | | 545 | | | | | 550 | |
| GAG | ATC | CCC | CAT | CGT | TCA | GGC | AAA | GCA | GCT | GGA | ACT | GAC | CCC | AAC | ATG | 2155 |
| 30Glu | Ile | Pro | His | Arg | Ser | Gly | Lys | Ala | Ala | Gly | Thr | Asp | Pro | Asn | Met | |
| | | | 555 | | | | | 560 | | | | | | 565 | | |
| GCT | GAC | AAT | GGG | GAC | CTG | GAC | CTG | GGG | CCG | GTA | GAG | ACA | GAA | CCA | CCC | 2203 |
| Ala | Asp | Asn | Gly | Asp | Leu | Asp | Leu | Gly | Pro | Val | Glu | Thr | Glu | Pro | Pro | |
| 35 | | | 570 | | | | | 575 | | | | | 580 | | | |
| TAT | GCC | TCA | CCT | AAA | TAC | CTC | CGC | AAT | TTC | ACT | CTG | ACT | GTC | ACA | GAC | 2251 |
| Tyr | Ala | Ser | Pro | Lys | Tyr | Leu | Arg | Asn | Phe | Thr | Leu | Thr | Val | Thr | Asp | |
| | | 585 | | | | | 590 | | | | | 595 | | | | |
| 40 | | | | | | | | | | | | | | | | |
| TGT | TAC | CGT | GGC | TGG | AAC | TCT | GCC | CCG | GGA | CGG | TTC | CAT | CTT | TTT | CCC | 2299 |
| Cys | Tyr | Arg | Gly | Trp | Asn | Ser | Ala | Pro | Gly | Arg | Phe | His | Leu | Phe | Pro | |
| | 600 | | | | | 605 | | | | | 610 | | | | | |
| 45CAC | ACA | CCC | TTT | GAT | CCT | GTG | TTG | CCC | TCT | GAG | GCC | AAA | TTC | TTG | GGC | 2347 |
| His | Thr | Pro | Phe | Asp | Pro | Val | Leu | Pro | Ser | Glu | Ala | Lys | Phe | Leu | Gly | |
| 615 | | | | | 620 | | | | | 625 | | | | | 630 | |
| TCA | GGG | ACT | GGA | TTT | CGG | CCG | ATC | GGT | GGC | GGG | GCT | GGG | GGC | TCT | GGC | 2395 |
| 50Ser | G | | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| | TGG | AAC | TCT | CCC | AAG | CTG | CCC | TCG | GAG | GAC | CTT | TTG | TGG | CCA | GAC | ATT | 2587 |
| | Trp | Asn | Ser | Pro | Lys | Leu | Pro | Ser | Glu | Asp | Leu | Leu | Trp | Pro | Asp | Ile | |
| | 695 | | | | | 700 | | | | | 705 | | | | | 710 | |
| 5 | GGT | GTC | CCC | ATC | ATG | GTC | GTC | CGT | ACT | GAG | AAG | AAC | AGT | TTG | AAC | AAT | 2635 |
| | Gly | Val | Pro | Ile | Met | Val | Val | Arg | Thr | Glu | Lys | Asn | Ser | Leu | Asn | Asn | |
| | | | | | 715 | | | | | 720 | | | | | | 725 | |
| | CGG | TTC | TTG | CCC | TGG | AAT | GAG | ATT | GAG | ACA | GAG | GCC | ATA | CTG | TCC | ATC | 2683 |
| 10 | Arg | Phe | Leu | Pro | Trp | Asn | Glu | Ile | Glu | Thr | Glu | Ala | Ile | Leu | Ser | Ile | |
| | | | | 730 | | | | | 735 | | | | | 740 | | | |
| | GAC | GAT | GAT | GCT | CAC | CTC | CGC | CAT | GAT | GAA | ATC | ATG | TTT | GGG | TTT | TGG | 2731 |
| 15 | Asp | Asp | Asp | Ala | His | Leu | Arg | His | Asp | Glu | Ile | Met | Phe | Gly | Phe | Trp | |
| | | | 745 | | | | | 750 | | | | | 755 | | | | |
| | GTG | TGG | AGA | GAA | GCA | CGT | GAT | CGC | ATT | GTG | GGT | TTC | CCT | GGC | CGG | TAC | 2779 |
| | Val | Trp | Arg | Glu | Ala | Arg | Asp | Arg | Ile | Val | Gly | Phe | Pro | Gly | Arg | Tyr | |
| | | 760 | | | | | 765 | | | | | 770 | | | | | |
| 20 | CAT | GCG | TGG | GAC | ATC | CCG | CAC | CAG | TCC | TGG | CTC | TAC | AAT | TCC | AAC | TAC | 2827 |
| | His | Ala | Trp | Asp | Ile | Pro | His | Gln | Ser | Trp | Leu | Tyr | Asn | Ser | Asn | Tyr | |
| | 775 | | | | | 780 | | | | | 785 | | | | | 790 | |
| 25 | TCC | TGT | GAG | CTG | TCC | ATG | GTG | CTG | ACG | GGC | GCT | GCC | TTC | TTT | CAC | AAG | 2875 |
| | Ser | Cys | Glu | Leu | Ser | Met | Val | Leu | Thr | Gly | Ala | Ala | Phe | Phe | His | Lys | |
| | | | | | 795 | | | | | 800 | | | | | 805 | | |
| | TAT | TAT | GCC | TAC | CTG | TAT | TCT | TAT | GTG | ATG | CCC | CAG | GCC | ATC | CGG | GAC | 2923 |
| 30 | Tyr | Tyr | Ala | Tyr | Leu | Tyr | Ser | Tyr | Val | Met | Pro | Gln | Ala | Ile | Arg | Asp | |
| | | | | 810 | | | | | 815 | | | | | 820 | | | |
| | ATG | GTG | GAC | GAG | TAC | ATC | AAC | TGT | GAG | GAT | ATC | GCC | ATG | AAC | TTC | CTT | 2971 |
| | Met | Val | Asp | Glu | Tyr | Ile | Asn | Cys | Glu | Asp | Ile | Ala | Met | Asn | Phe | Leu | |
| 35 | | | 825 | | | | | 830 | | | | | 835 | | | | |
| | GTC | TCC | CAC | ATC | ACA | CGG | AAA | CCC | CCC | ATC | AAG | GTG | ACA | TCA | AGG | TGG | 3019 |
| | Val | Ser | His | Ile | Thr | Arg | Lys | Pro | Pro | Ile | Lys | Val | Thr | Ser | Arg | Trp | |
| | | | 840 | | | | 845 | | | | | 850 | | | | | |
| 40 | ACT | TTT | CGA | TGC | CCA | GGG | TGC | CCT | CAG | GCC | CTG | TCC | CAT | GAT | GAC | TCT | 3067 |
| | Thr | Phe | Arg | Cys | Pro | Gly | Cys | Pro | Gln | Ala | Leu | Ser | His | Asp | Asp | Ser | |
| | 855 | | | | | 860 | | | | | 865 | | | | | 870 | |
| 45 | CAT | TTT | CAC | GAG | CGG | CAC | AAG | TGT | ATC | AAC | TTT | TTT | GTG | AAG | GTG | TAC | 3115 |
| | His | Phe | His | Glu | Arg | His | Lys | Cys | Ile | Asn | Phe | Phe | Val | Lys | Val | Tyr | |
| | | | | | 875 | | | | | 880 | | | | | 885 | | |
| | GGC | TAT | ATG | CCT | CTC | TTG | TAC | ACA | CAG | TTC | AGG | GTG | GAC | TCC | GTG | CTC | 3163 |
| 50 | Gly | Tyr | Met | | | | | | | | | | | | | | |

ACTGAGGACT GTTCATAAGC CCAGGACA

3479

(2) INFORMATION FOR SEQ ID NO:2:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 918 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

10

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

15 Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly
 1 5 10 15
 Gln Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu
 20 25 30
 20 Ser Phe Thr Leu Phe Ile Ile Leu Val Phe Phe Pro Leu Ile Ala His
 35 40 45
 Tyr Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile
 25 50 55 60
 Phe Gly Pro Arg Ala Gly Ser Glu Leu Cys Glu Val Lys His Val Leu
 65 70 75 80
 30 Asp Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu
 85 90 95
 Glu Ala Lys Arg Gln Glu Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu
 100 105 110
 35 Lys Ile Glu Ala Cys Lys Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu
 115 120 125
 Leu Gln Leu Lys Asn Val Ile Ser Gln Thr Glu His Ser Tyr Lys Glu
 40 130 135 140
 Leu Met Ala Gln Asn Gln Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu
 145 150 155 160
 45 Pro Glu Lys Asp Asp Ala Gly Leu Pro Pro Pro Lys Val Thr Arg Gly
 165 170 175
 Cys Arg Leu His Asn Cys Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser
 180 185 190
 50 Gly Phe Pro Val Tyr Val Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser
 195 200 205
 Tyr Leu Asp Pro Leu Val Lys Gln Ala Phe Gln Ala Thr Val Arg Ala
 55 210 215 220
 Asn Val Tyr Val Thr Glu Asn Ala Ala Ile Ala Cys Leu Tyr Val Val
 225 230 235 240
 60 Leu Val Gly Glu Met Gln Glu Pro Thr Val Leu Arg Pro Ala Asp Leu
 245 250 255
 Glu Lys Gln Leu Phe Ser Leu Pro His Trp Arg Thr Asp Gly His Asn

TOGETHER 02560850

[illegible]

595 600 605

Arg Phe His Leu Phe Pro His Thr Pro Phe Asp Pro Val Leu Pro Ser
610 615 620

5
Glu Ala Lys Phe Leu Gly Ser Gly Thr Gly Phe Arg Pro Ile Gly Gly
625 630 635 640

10
Gly Ala Gly Gly Ser Gly Lys Glu Phe Gln Ala Ala Leu Gly Gly Asn
645 650 655

Val Gln Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg Glu
660 665 670

15
Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr Leu
675 680 685

Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp
690 695 700

20
Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr Glu
705 710 715 720

25
Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr
725 730 735

Glu Ala Ile Leu Ser Ile Asp Asp Ala His Leu Arg His Asp Glu
740 745 750

30
Ile Met Phe Gly Phe Trp Val Trp Arg Glu Ala Arg Asp Arg Ile Val
755 760 765

Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser Trp
770 775 780

35
Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr Gly
785 790 795 800

40
Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met
805 810 815

Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu Asp
820 825 830

45
Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro Ile
835 840 845

Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala
850 855 860

50
Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn
865 870 875 880

Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe
885 890 895

55
Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr
900 905 910

60
Lys Cys Phe Lys Phe Ile
915

(2) INFORMATION FOR SEQ ID NO:3:

09809920.031601

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6172 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

10 (ix) FEATURE:

- (A) NAME/KEY: CDS
 (B) LOCATION: 594..3350

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCGGGTCCC TGAGCTGGAA GCCGGAGAGC AAGCCCTGGA GGTTCACTCT TTCAAGAAGT 60
 CGTGTGCTGA GGTGTAATGC TACACAAGTC AGAGGAAGGA AGGGTCCTGA AACACATGGC 120
 20 CTGATTGTTG GCAAAGGCAT CATAAGAAGC TGGCATTAT TTCTGTTCTA ACCTATTACT 180
 GTATAACTGT GAATAGACAC TATGCATATT TGTTGGTCAG CAAAACCAAG AAACAAGAGC 240
 25 TATGGCATTT GAAAAAGTCT GTCTGATTCC AGGGTGTTTT TCCTGGGTTT CATCATCAGG 300
 TACCTCCTCC CTTTCATCTC AGCAAGAATG TGGCACCTTT TATCGTTTGA TAAAGATTAA 360
 GGACATGTTT TTTGGTCAAC AGCCAGAACT TAAATCTGC TGGAATAGGG TCAGAGACCA 420
 30 TTTCAGCTGC AGCTGAGGAA AATGAAATGT TCATTTTATT TGGTGCCTTG TCTGGGGAGC 480
 AACTAACTC TTCTGGAAAC GTGTCAGTGA AACAGAGATC GTTTTGTGGA ATAGCAACCC 540
 35 ATGTTATGG CGAGTGACCC GACGTGATCT GGGGGGCAGG CTGCAGAGGA CTC ATG 596
 Met
 ACA GGC TAT ACC ATG CTG CGG AAT GGG GGC GCG GGG AAC GGA GGT CAG 644
 40 Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Ala Gly Asn Gly Gly Gln 920 925 930 935
 ACC TGC ATG CTG CGC TGG TCC AAC CGC ATC CGC CTC ACG TGG CTC AGC 692
 45 Thr Cys Met Leu Arg Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser 940 945 950
 TTC ACG CTC TTT GTC ATC CTG GTC TTC TTC CCG CTC ATC GCC CAC TAT 740
 Phe Thr Leu Phe Val Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr 955 960 965
 50 TAC CTC ACC ACT CTG GAT GAG GCT GAT GAG GCA GGC AAG CGG ATT TTT 788
 Tyr Leu Thr Thr Leu Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe 970 975 980
 55 GGT CCC CGG GTG GGG AAC GAG CTG TGC GAG GTG AAG CAC GTG CTG GAT 836
 Gly Pro Arg Val Gly Asn Glu Leu Cys Glu Val Lys His Val Leu Asp 985 990 995
 CTG TGC CGC ATC CGG GAG TCG GTG AGT GAA GAG CTC CTG CAG CTG GAG 884
 60 Leu Cys Arg Ile Arg Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu 1000 1005 1010 1015
 GCC AAG CGC CAA GAG CTG AAC AGC GAG ATC GCC AAG CTG AAT CTG AAG 932

TOTAL: 02660860

| | Ala | Lys | Arg | Gln | Glu | Leu | Asn | Ser | Glu | Ile | Ala | Lys | Leu | Asn | Leu | Lys | |
|----|------|------|------|------|-----|------|------|------|------|------|------|------|------|------|------|------|------|
| | 1020 | | | | | | | | 1025 | | | | 1030 | | | | |
| 5 | ATC | GAA | GCC | TGT | AAG | AAG | AGC | ATT | GAG | AAC | GCC | AAG | CAG | GAC | CTG | CTC | 980 |
| | Site | Glu | Ala | Cys | Lys | Lys | Ser | Ile | Glu | Asn | Ala | Lys | Gln | Asp | Leu | Leu | |
| | | | | 1035 | | | | | 1040 | | | | | 1045 | | | |
| 10 | CAG | CTC | AAG | AAT | GTC | ATC | AGC | CAG | ACC | GAG | CAT | TCC | TAC | AAG | GAG | CTC | 1028 |
| | Gln | Leu | Lys | Asn | Val | Ile | Ser | Gln | Thr | Glu | His | Ser | Tyr | Lys | Glu | Leu | |
| | | | 1050 | | | | | 1055 | | | | | 1060 | | | | |
| 15 | ATG | GCC | CAG | AAC | CAG | CCC | AAG | CTG | TCC | CTG | CCC | ATC | CGA | CTG | CTC | CCA | 1076 |
| | Met | Ala | Gln | Asn | Gln | Pro | Lys | Leu | Ser | Leu | Pro | Ile | Arg | Leu | Leu | Pro | |
| | | 1065 | | | | | 1070 | | | | | 1075 | | | | | |
| 20 | GAG | AAG | GAC | GAT | GCC | GGC | CTC | CCT | CCC | CCG | AAG | GCC | ACT | CGG | GGC | TGC | 1124 |
| | Glu | Lys | Asp | Asp | Ala | Gly | Leu | Pro | Pro | Pro | Lys | Ala | Thr | Arg | Gly | Cys | |
| | 1080 | | | | | 1085 | | | | | 1090 | | | | | 1095 | |
| 25 | CGG | CTA | CAC | AAC | TGC | TTT | GAT | TAT | TCT | CGT | TGC | CCT | CTC | ACC | TCT | GGC | 1172 |
| | Arg | Leu | His | Asn | Cys | Phe | Asp | Tyr | Ser | Arg | Cys | Pro | Leu | Thr | Ser | Gly | |
| | | | | 1100 | | | | | | 1105 | | | | | 1110 | | |
| 30 | TTC | CCG | GTC | TAC | GTC | TAT | GAC | AGT | GAC | CAG | TTT | GTC | TTT | GGC | AGC | TAC | 1220 |
| | Phe | Pro | Val | Tyr | Val | Tyr | Asp | Ser | Asp | Gln | Phe | Val | Phe | Gly | Ser | Tyr | |
| | | | | 1115 | | | | | 1120 | | | | | 1125 | | | |
| 35 | CTG | GAT | CCC | TTG | GTC | AAG | CAG | GCT | TTT | CAG | GCG | ACA | GCA | CGA | GCT | AAC | 1268 |
| | Leu | Asp | Pro | Leu | Val | Lys | Gln | Ala | Phe | Gln | Ala | Thr | Ala | Arg | Ala | Asn | |
| | | | 1130 | | | | | 1135 | | | | | 1140 | | | | |
| 40 | GTT | TAT | GTT | ACA | GAA | AAT | GCA | GAC | ATC | GCC | TGC | CTT | TAC | GTG | ATA | CTA | 1316 |
| | Val | Tyr | Val | Thr | Glu | Asn | Ala | Asp | Ile | Ala | Cys | Leu | Tyr | Val | Ile | Leu | |
| | | 1145 | | | | | 1150 | | | | | 1155 | | | | | |
| 45 | GTG | GGA | GAG | ATG | CAG | GAG | CCC | GTG | GTG | CTG | CGG | CCT | GCT | GAG | CTG | GAG | 1364 |
| | Val | Gly | Glu | Met | Gln | Glu | Pro | Val | Val | Leu | Arg | Pro | Ala | Glu | Leu | Glu | |
| | 1160 | | | | | 1165 | | | | | 1170 | | | | | 1175 | |
| 50 | AAG | CAG | TTG | TAT | TCC | CTG | CCA | CAC | TGG | CGG | ACG | GAT | GGA | CAC | AAC | CAT | 1412 |
| | Lys | Gln | Leu | Tyr | Ser | Leu | Pro | His | Trp | Arg | Thr | Asp | Gly | His | Asn | His | |
| | | | | 1180 | | | | | 1185 | | | | | 1190 | | | |
| 55 | GTC | ATC | ATC | AAT | CTG | TCA | CGT | AAG | TCA | GAT | ACA | CAG | AAC | CTT | CTC | TAT | 1460 |
| | Val | Ile | Ile | Asn | Leu | Ser | Arg | Lys | Ser | Asp | Thr | Gln | Asn | Leu | Leu | Tyr | |
| | | | | 1195 | | | | 1200 | | | | | | 1205 | | | |
| 60 | AAC | GTC | AGT | ACT | GGC | CGT | GCC | ATG | GTG | GCC | CAG | TCC | ACC | TTC | TAC | ACT | 1508 |
| | Asn | Val | Ser | Thr | Gly | Arg | Ala | Met | Val | Ala | Gln | Ser | Thr | Phe | Tyr | Thr | |
| | | | 1210 | | | | | | | | | | | | | | |

| | | | | | | | | | | | | | | | | | |
|----|-------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| | AGG | TCT | AGC | CTT | CAG | GAG | GCC | CGC | TCC | TTC | GAA | GAG | GAA | ATG | GAG | GGC | 1700 |
| | Arg | Ser | Ser | Leu | Gln | Glu | Ala | Arg | Ser | Phe | Glu | Glu | Glu | Met | Glu | Gly | |
| | | | | 1275 | | | | | 1280 | | | | | 1285 | | | |
| | 5GAC | CCT | CCC | GCC | GAC | TAC | GAT | GAC | CGG | ATC | ATT | GCC | ACC | CTG | AAG | GCG | 1748 |
| | Asp | Pro | Pro | Ala | Asp | Tyr | Asp | Asp | Arg | Ile | Ile | Ala | Thr | Leu | Lys | Ala | |
| | | | 1290 | | | | | 1295 | | | | | 1300 | | | | |
| | GTG | CAG | GAC | AGC | AAG | CTG | GAT | CAG | GTC | CTG | GTG | GAA | TTC | ACC | TGC | AAA | 1796 |
| 10 | Val | Gln | Asp | Ser | Lys | Leu | Asp | Gln | Val | Leu | Val | Glu | Phe | Thr | Cys | Lys | |
| | | 1305 | | | | | 1310 | | | | | 1315 | | | | | |
| | AAC | CAG | CCC | AAA | CCC | AGC | CTG | CCG | ACT | GAG | TGG | GCA | CTG | TGT | GGA | GAG | 1844 |
| | Asn | Gln | Pro | Lys | Pro | Ser | Leu | Pro | Thr | Glu | Trp | Ala | Leu | Cys | Gly | Glu | |
| 15 | 1320 | | | | | 1325 | | | | 1330 | | | | | | 1335 | |
| | CGG | GAG | GAC | CGC | TTG | GAA | TTG | CTG | AAG | CTC | TCC | ACC | TTC | GCC | CTC | ATC | 1892 |
| | Arg | Glu | Asp | Arg | Leu | Glu | Leu | Leu | Lys | Leu | Ser | Thr | Phe | Ala | Leu | Ile | |
| | | | | 1340 | | | | | | 1345 | | | | | 1350 | | |
| 20 | ATT | ACC | CCC | GGG | GAC | CCT | CGC | TTG | GTT | ATT | TCC | TCT | GGG | TGT | GCA | ACA | 1940 |
| | Ile | Thr | Pro | Gly | Asp | Pro | Arg | Leu | Val | Ile | Ser | Ser | Gly | Cys | Ala | Thr | |
| | | | | 1355 | | | | 1360 | | | | | | 1365 | | | |
| | 25CGG | CTC | TTC | GAA | GCC | CTG | GAA | GTC | GGT | GCC | GTC | CCG | GTG | GTG | CTG | GGG | 1988 |
| | Arg | Leu | Phe | Glu | Ala | Leu | Glu | Val | Gly | Ala | Val | Pro | Val | Val | Leu | Gly | |
| | | | 1370 | | | | | 1375 | | | | 1380 | | | | | |
| | GAG | CAG | GTC | CAG | CTT | CCC | TAC | CAG | GAC | ATG | CTG | CAG | TGG | AAC | GAG | GCG | 2036 |
| 30 | Glu | Gln | Val | Gln | Leu | Pro | Tyr | Gln | Asp | Met | Leu | Gln | Trp | Asn | Glu | Ala | |
| | | 1385 | | | | | 1390 | | | | | 1395 | | | | | |
| | GCC | CTG | GTG | GTG | CCA | AAG | CCT | CGT | GTT | ACC | GAG | GTT | CAT | TTC | CTG | CTC | 2084 |
| | Ala | Leu | Val | Val | Pro | Lys | Pro | Arg | Val | Thr | Glu | Val | His | Phe | Leu | Leu | |
| 35 | 1400 | | | | | 1405 | | | | | 1410 | | | | | 1415 | |
| | AGA | AGC | CTC | TCC | GAT | AGT | GAC | CTC | CTG | GCT | ATG | AGG | CGG | CAA | GGC | CGC | 2132 |
| | Arg | Ser | Leu | Ser | Asp | Ser | Asp | Leu | Leu | Ala | Met | Arg | Arg | Gln | Gly | Arg | |
| | | | | | 1420 | | | | | 1425 | | | | | 1430 | | |
| 40 | TTT | CTC | TGG | GAG | ACT | TAC | TTC | TCC | ACT | GCT | GAC | AGT | ATT | TTT | AAT | ACC | 2180 |
| | Phe | Leu | Trp | Glu | Thr | Tyr | Phe | Ser | Thr | Ala | Asp | Ser | Ile | Phe | Asn | Thr | |
| | | | | 1435 | | | | 1440 | | | | | | 1445 | | | |
| | 45GTG | CTG | GCT | ATG | ATT | AGG | ACT | CGC | ATC | CAG | ATC | CCA | GCC | GCT | CCC | ATC | 2228 |
| | Val | Leu | Ala | Met | Ile | Arg | Thr | Arg | Ile | Gln | Ile | Pro | Ala | Ala | Pro | Ile | |
| | | | 1450 | | | | | 1455 | | | | 1460 | | | | | |
| | CGG | GAA | GAG | GCG | GCA | GCT | GAG | ATC | CCC | CAC | CGT | TCA | GGC | AAG | GCG | GCT | 2276 |
| 50 | Arg | Glu | Glu | Ala | Ala | Ala | Glu | Ile | Pro | His | Arg | Ser | Gly | Lys | Ala | Ala | |
| | | 1465 | | | | | 1470 | | | | | 1475 | | | | | |
| | GGA | ACT | GAC | CCC | AAC | ATG | GCT | GAC | AAC | GGG | GAC | CTG | GAC | CTG | GGG | CCA | 2324 |
| | Gly | Thr | Asp | Pro | Asn | Met | Ala | Asp | Asn | Gly | Asp | Leu | Asp | Leu | Gly | Pro | |
| 55 | 1480 | | | | | 1485 | | | | 1490 | | | | | | 1495 | |
| | GTG | GAG | ACG | GAG | CCG | CCC | TAC | GCC | TCA | CCC | AGA | TAC | CTC | CGC | AAT | TTC | 2372 |
| | Val | Glu | Thr | Glu | Pro | Pro | Tyr | Ala | Ser | Pro | Arg | Tyr | Leu | Arg | Asn | Phe | |
| | | | | | 1500 | | | | | 1505 | | | | | 1510 | | |
| 60 | ACT | CTG | ACT | GTC | ACT | GAC | TTT | TAC | CGC | AGC | TGG | AAC | TGT | GCT | CCA | GGG | 2420 |
| | Thr | Leu | Thr | Val | Thr | Asp | Phe | Tyr | Arg | Ser | Trp | Asn | Cys | Ala | Pro | Gly | |
| | | | | 1515 | | | | 1520 | | | | | | 1525 | | | |

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| | | | | | | | | | | | | | | | | | |
|----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
| | CCT | TTC | CAT | CTT | TTC | CCC | CAC | ACT | CCC | TTT | GAC | CCT | GTG | TTG | CCC | TCA | 2468 |
| | Pro | Phe | His | Leu | Phe | Pro | His | Thr | Pro | Phe | Asp | Pro | Val | Leu | Pro | Ser | |
| | | | 1530 | | | | | 1535 | | | | | 1540 | | | | |
| 5 | GAG | GCC | AAA | TTC | TTG | GGC | TCA | GGG | ACT | GGC | TTT | CGG | CCT | ATT | GGT | GGT | 2516 |
| | Glu | Ala | Lys | Phe | Leu | Gly | Ser | Gly | Thr | Gly | Phe | Arg | Pro | Ile | Gly | Gly | |
| | | 1545 | | | | 1550 | | | | | 1555 | | | | | | |
| | GGA | GCT | GGG | GGT | TCT | GGC | AAG | GAA | TTT | CAG | GCA | GCG | CTT | GGA | GGC | AAT | 2564 |
| 10 | Gly | Ala | Gly | Gly | Ser | Gly | Lys | Glu | Phe | Gln | Ala | Ala | Leu | Gly | Gly | Asn | |
| | | 1560 | | | | 1565 | | | | 1570 | | | | | | 1575 | |
| | GTT | CCC | CGA | GAG | CAG | TTC | ACG | GTG | GTG | ATG | TTG | ACT | TAT | GAG | CGG | GAG | 2612 |
| 15 | Val | Pro | Arg | Glu | Gln | Phe | Thr | Val | Val | Met | Leu | Thr | Tyr | Glu | Arg | Glu | |
| | | | | | 1580 | | | | | 1585 | | | | 1590 | | | |
| | GAA | GTG | CTT | ATG | AAC | TCT | TTA | GAG | AGG | CTG | AAT | GGC | CTC | CCT | TAC | CTG | 2660 |
| | Glu | Val | Leu | Met | Asn | Ser | Leu | Glu | Arg | Leu | Asn | Gly | Leu | Pro | Tyr | Leu | |
| | | | | 1595 | | | | 1600 | | | | | 1605 | | | | |
| 20 | AAC | AAG | GTC | GTG | GTG | GTG | TGG | AAT | TCT | CCC | AAG | CTG | CCA | TCA | GAG | GAC | 2708 |
| | Asn | Lys | Val | Val | Val | Val | Trp | Asn | Ser | Pro | Lys | Leu | Pro | Ser | Glu | Asp | |
| | | 1610 | | | | | | 1615 | | | | 1620 | | | | | |
| 25 | CTT | CTG | TGG | CCT | GAC | ATT | GGC | GTT | CCC | ATC | ATG | GTG | GTC | CGT | ACT | GAG | 2756 |
| | Leu | Leu | Trp | Pro | Asp | Ile | Gly | Val | Pro | Ile | Met | Val | Val | Arg | Thr | Glu | |
| | | 1625 | | | | | 1630 | | | | | 1635 | | | | | |
| | AAG | AAC | AGT | TTG | AAC | AAC | CGA | TTC | TTA | CCC | TGG | AAT | GAA | ATT | GAG | ACA | 2804 |
| 30 | Lys | Asn | Ser | Leu | Asn | Asn | Arg | Phe | Leu | Pro | Trp | Asn | Glu | Ile | Glu | Thr | |
| | | 1640 | | | | 1645 | | | | | 1650 | | | | 1655 | | |
| | GAG | GCC | ATC | CTG | TCC | ATT | GAT | GAC | GAT | GCT | CAC | CTC | CGC | CAT | GAC | GAA | 2852 |
| 35 | Glu | Ala | Ile | Leu | Ser | Ile | Asp | Asp | Asp | Ala | His | Leu | Arg | His | Asp | Glu | |
| | | | | 1660 | | | | 1665 | | | | | 1670 | | | | |
| | ATC | ATG | TTT | GGG | TTC | CGG | GTG | TGG | AGA | GAA | GCT | CGG | GAC | CGC | ATC | GTG | 2900 |
| | Ile | Met | Phe | Gly | Phe | Arg | Val | Trp | Arg | Glu | Ala | Arg | Asp | Arg | Ile | Val | |
| | | | | 1675 | | | | 1680 | | | | | 1685 | | | | |
| 40 | GGC | TTC | CCT | GGC | CGT | TAC | CAC | GCA | TGG | GAC | ATC | CCC | CAT | CAG | TCC | TGG | 2948 |
| | Gly | Phe | Pro | Gly | Arg | Tyr | His | Ala | Trp | Asp | Ile | Pro | His | Gln | Ser | Trp | |
| | | | 1690 | | | | | 1695 | | | | | 1700 | | | | |
| 45 | CTC | TAC | AAC | TCC | AAC | TAC | TCC | TGT | GAG | CTG | TCC | ATG | GTG | CTG | ACA | GGT | 2996 |
| | Leu | Tyr | Asn | Ser | Asn | Tyr | Ser | Cys | Glu | Leu | Ser | Met | Val | Leu | Thr | Gly | |
| | | 1705 | | | | | 1710 | | | | | 1715 | | | | | |
| | GCT | GCC | TTC | TTT | CAC | AAG | TAT | TAT | GCC | TAC | CTG | TAT | TCT | TAT | GTG | ATG | 3044 |
| 50 | Ala | Ala | Phe | Phe | His | Lys | Tyr | Tyr | Ala | Tyr | Leu | Tyr | Ser | Tyr | Val | Met | |
| | | 1720 | | | | 1725 | | | | | 1730 | | | | | 1735 | |
| | CCC | CAG | GCC | ATC | CGG | GAC | ATG | GTG | GAT | GAA | TAC | ATC | AAC | TGT | GAG | GAC | 3092 |
| 55 | Pro | Gln | Ala | Ile | Arg | Asp | Met | Val | Asp | Glu | Tyr | Ile | Asn | Cys | Glu | Asp | |
| | | | | 1740 | | | | | 1745 | | | | | | 1750 | | |
| | ATT | GCC | ATG | AAC | TTC | CTT | GTC | TCC | CAC | ATC | ACT | CGG | AAG | CCC | CCC | ATC | 3140 |
| | Ile | Ala | Met | Asn | Phe | Leu | Val | Ser | His | Ile | Thr | Arg | Lys | Pro | Pro | Ile | |
| | | | | 1755 | | | | 1760 | | | | | 1765 | | | | |
| 60 | AAG | GTG | ACC | TCA | CGG | TGG | ACA | TTC | CGA | TGC | CCA | GGA | TGC | CCT | CAG | GCC | 3188 |
| | Lys | Val | Thr | Ser | Arg | Trp | Thr | Phe | Arg | Cys | Pro | Gly | Cys | Pro | Gln | Ala | |
| | | 1770 | | | | | | 1775 | | | | | 1780 | | | | |

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| | | |
|----|--|------|
| | CTG TCT CAT GAT GAC TCC CAC TTC CAC GAG CGG CAC AAG TGC ATC AAC | 3236 |
| | Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn | |
| | 1785 1790 1795 | |
| 5 | TTC TTC GTG AAG GTG TAC GGC TAC ATG CCC CTC CTG TAC ACG CAG TTC | 3284 |
| | Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe | |
| | 1800 1805 1810 1815 | |
| | AGG GTG GAT TCT GTG CTC TTC AAG ACA CGC CTG CCC CAT GAC AAG ACC | 3332 |
| 10 | Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr | |
| | 1820 1825 1830 | |
| | AAG TGC TTC AAG TTC ATC TAGGGGCAGC GCACGGTCTG GGGAAAGAGGA | 3380 |
| | Lys Cys Phe Lys Phe Ile | |
| 15 | 1835 | |
| | TGAGCAGAGG GAGGAAGATG GCTCCCAAGG TTCCTAGGCA TTGCAGGACC TTGGGCACAT | 3440 |
| | CTGCTGGTGG GTGGCCCAGA GCCTCTGCTG GAAGGGGCAG CAGGAGGAGT GGAAGGAAAC | 3500 |
| 20 | CGCTGCCTTT ATCTTGAAGT CAGCCACACT GGGCCTGGAG CCCTGGGCGG AGTCCCCGGG | 3560 |
| | GTTCCCCACA CAGGGCACTG ACTGATAGCT TACACTGAGG ACTGTGGCGA CTCTGCAGAG | 3620 |
| 25 | TCACTCACAC CGTTCGTACG CCCAGGACAG CTGGTTCGTG GTTTTTACAT TCAATAACAA | 3680 |
| | CTATTATGAT TATTTAAAAA GAGAAAGTTT CAGATTTGCC ATTCAAGGCT TATTTATATA | 3740 |
| | TATGTGTGTG TATATAAATA CATGCACACA CTTGCATACA TATATATTTT TGGCTGGGGG | 3800 |
| 30 | AGTGTGAGTT TTGCCTTTCT AAGGGAGGGA CCGCGCAGGC TCCTTTGTTC TGTATTCTGG | 3860 |
| | CGGAGATGGG TCCTGGCCTT GTGTCACTGG CTTATCCTTA AAGATCATCT CCCATCCTCC | 3920 |
| 35 | CCAGCGCCAT CTGTGTGCAG CAACCAGAAA GGGATGAACT TGGCCCTCTT GCGGGCCTGG | 3980 |
| | ACAAGGTCTC TTCCTTACCC TTTCTGTTGC CAGTCAGCAA CCTGTAACTC ACATTCTCTT | 4040 |
| | CCCAGTGAAT CCCTGGGAGC GCCTGACCCT GGTGGGCTGT TCAGCTTCCT GCTGCTGGGG | 4100 |
| 40 | CCAGCGATTT TTGAGGATTT ATCTTTAGGC CAGGCTTGCC TCCGTA CTTA TCCCTGCTCT | 4160 |
| | CCCATTCTC TCTTGTTTGA GAGAGAATGA GGAAGCAAAG AGTGAGAAAAG AATAGGGGCT | 4220 |
| 45 | GAAGACGCCA CTCCCAGATG GCTCTTTCTA TCCTGCTCTT CTGTTGAAAC ACACGTGCTG | 4280 |
| | TGGGCCTCAG GCGTTTCTGA AGTGCTCTTT CTTGGATTGG ACAGGAGATC AGCAGCGTGC | 4340 |
| | ACATCTGCTG TGGTCTGAAG TGGTTTGCAG GTCAGCCTCC TCTCCCTAGT GTAGAGCAAG | 4400 |
| 50 | CCAGTGCCT TCGAGGAACC CACCCGGCTG GCCGGGAAGT TTTACAGCAA GGC GCCTGCC | 4460 |
| | TTGGGATAAT TCCTTGGTGA AATTCACCTT CCCCCGCT CTGTCTGGAG CCCATCCTG | 4520 |
| 55 | TGTTATCTGT GGT TTTTGA CCCCTAATGT CAGCTTGGCT GTAGGACTCC CCGAGGTTTG | 4580 |
| | GTATGTGCTA GAACAATGGG AGGCTGTGAT TTGCTGTGTA AGCTCACATC CAGCCTTGA | 4640 |
| | ATCTAACGGG CATTCAACAAC CCGAGTTACC ACTTTCCACT CCCTGCTTAG GATTCTGTTC | 4700 |
| 60 | CCTGGGCTGA AACTGAAATA AGCTAATTTT TTGGGTCACG GTGGCAGTAG GGGAACCTAG | 4760 |
| | GAGGGTGTGA GTGGCATTG TCAGGGATTT AGCCCATGAC GTGTTTCTTG AACCTACTT | 4820 |

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(2) INFORMATION FOR SEQ ID NO:4:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 919 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Thr | Gly | Tyr | Thr | Met | Leu | Arg | Asn | Gly | Gly | Ala | Gly | Asn | Gly | Gly |
| 60 | 1 | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Thr | Cys | Met | Leu | Arg | Trp | Ser | Asn | Arg | Ile | Arg | Leu | Thr | Trp | Leu |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | Ser | Phe | Thr | Leu | Phe | Val | Ile | Leu | Val | Phe | Phe | Pro | Leu | Ile | Ala | His |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | | | | 35 | | | | 40 | | | | | 45 | | | |
| 5 | Tyr | Tyr | Leu | Thr | Thr | Leu | Asp | Glu | Ala | Asp | Glu | Ala | Gly | Lys | Arg | Ile |
| | | 50 | | | | | 55 | | | | | 60 | | | | |
| | Phe | Gly | Pro | Arg | Val | Gly | Asn | Glu | Leu | Cys | Glu | Val | Lys | His | Val | Leu |
| | 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| 10 | Asp | Leu | Cys | Arg | Ile | Arg | Glu | Ser | Val | Ser | Glu | Glu | Leu | Leu | Gln | Leu |
| | | | | | 85 | | | | | 90 | | | | | 95 | |
| | Glu | Ala | Lys | Arg | Gln | Glu | Leu | Asn | Ser | Glu | Ile | Ala | Lys | Leu | Asn | Leu |
| | | | | 100 | | | | | 105 | | | | | 110 | | |
| 15 | Lys | Ile | Glu | Ala | Cys | Lys | Lys | Ser | Ile | Glu | Asn | Ala | Lys | Gln | Asp | Leu |
| | | | 115 | | | | | 120 | | | | | 125 | | | |
| 20 | Leu | Gln | Leu | Lys | Asn | Val | Ile | Ser | Gln | Thr | Glu | His | Ser | Tyr | Lys | Glu |
| | 130 | | | | | | 135 | | | | | 140 | | | | |
| | Leu | Met | Ala | Gln | Asn | Gln | Pro | Lys | Leu | Ser | Leu | Pro | Ile | Arg | Leu | Leu |
| | 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| 25 | Pro | Glu | Lys | Asp | Asp | Ala | Gly | Leu | Pro | Pro | Pro | Lys | Ala | Thr | Arg | Gly |
| | | | | | 165 | | | | | 170 | | | | | 175 | |
| | Cys | Arg | Leu | His | Asn | Cys | Phe | Asp | Tyr | Ser | Arg | Cys | Pro | Leu | Thr | Ser |
| | | | | 180 | | | | | 185 | | | | | 190 | | |
| 30 | Gly | Phe | Pro | Val | Tyr | Val | Tyr | Asp | Ser | Asp | Gln | Phe | Val | Phe | Gly | Ser |
| | | | 195 | | | | | 200 | | | | | 205 | | | |
| 35 | Tyr | Leu | Asp | Pro | Leu | Val | Lys | Gln | Ala | Phe | Gln | Ala | Thr | Ala | Arg | Ala |
| | 210 | | | | | | 215 | | | | | 220 | | | | |
| | Asn | Val | Tyr | Val | Thr | Glu | Asn | Ala | Asp | Ile | Ala | Cys | Leu | Tyr | Val | Ile |
| | 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| 40 | Leu | Val | Gly | Glu | Met | Gln | Glu | Pro | Val | Val | Leu | Arg | Pro | Ala | Glu | Leu |
| | | | | | 245 | | | | | 250 | | | | | 255 | |
| | Glu | Lys | Gln | Leu | Tyr | Ser | Leu | Pro | His | Trp | Arg | Thr | Asp | Gly | His | Asn |
| | | | | 260 | | | | | 265 | | | | | 270 | | |
| 45 | His | Val | Ile | Ile | Asn | Leu | Ser | Arg | Lys | Ser | Asp | Thr | Gln | Asn | Leu | Leu |
| | | | 275 | | | | | 280 | | | | | 285 | | | |
| 50 | Tyr | Asn | Val | Ser | Thr | Gly | Arg | Ala | Met | Val | Ala | Gln | Ser | Thr | Phe | Tyr |
| | 290 | | | | | | 295 | | | | | 300 | | | | |
| | Thr | Val | Gln | Tyr | Arg | Pro | Gly | Phe | Asp | Leu | Val | Val | | | | |

| | Gly | Asp | Pro | Pro | Ala | Asp | Tyr | Asp | Asp | Arg | Ile | Ile | Ala | Thr | Leu | Lys |
|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 370 | | | | | | 375 | | | | | | 380 | | | |
| | Ala | Val | Gln | Asp | Ser | Lys | Leu | Asp | Gln | Val | Leu | Val | Glu | Phe | Thr | Cys |
| 5 | 385 | | | | | 390 | | | | | 395 | | | | | 400 |
| | Lys | Asn | Gln | Pro | Lys | Pro | Ser | Leu | Pro | Thr | Glu | Trp | Ala | Leu | Cys | Gly |
| | | | | | 405 | | | | | 410 | | | | | 415 | |
| 10 | Glu | Arg | Glu | Asp | Arg | Leu | Glu | Leu | Leu | Lys | Leu | Ser | Thr | Phe | Ala | Leu |
| | | | | 420 | | | | | 425 | | | | | 430 | | |
| | Ile | Ile | Thr | Pro | Gly | Asp | Pro | Arg | Leu | Val | Ile | Ser | Ser | Gly | Cys | Ala |
| 15 | | | 435 | | | | | 440 | | | | | 445 | | | |
| | Thr | Arg | Leu | Phe | Glu | Ala | Leu | Glu | Val | Gly | Ala | Val | Pro | Val | Val | Leu |
| | | 450 | | | | | 455 | | | | | 460 | | | | |
| | Gly | Glu | Gln | Val | Gln | Leu | Pro | Tyr | Gln | Asp | Met | Leu | Gln | Trp | Asn | Glu |
| 20 | 465 | | | | | 470 | | | | | 475 | | | | | 480 |
| | Ala | Ala | Leu | Val | Val | Pro | Lys | Pro | Arg | Val | Thr | Glu | Val | His | Phe | Leu |
| | | | | | 485 | | | | | 490 | | | | | 495 | |
| 25 | Leu | Arg | Ser | Leu | Ser | Asp | Ser | Asp | Leu | Leu | Ala | Met | Arg | Arg | Gln | Gly |
| | | | | 500 | | | | | 505 | | | | | 510 | | |
| | Arg | Phe | Leu | Trp | Glu | Thr | Tyr | Phe | Ser | Thr | Ala | Asp | Ser | Ile | Phe | Asn |
| 30 | | | 515 | | | | | 520 | | | | | 525 | | | |
| | Thr | Val | Leu | Ala | Met | Ile | Arg | Thr | Arg | Ile | Gln | Ile | Pro | Ala | Ala | Pro |
| | | 530 | | | | | 535 | | | | | 540 | | | | |
| | Ile | Arg | Glu | Glu | Ala | Ala | Ala | Glu | Ile | Pro | His | Arg | Ser | Gly | Lys | Ala |
| 35 | 545 | | | | | 550 | | | | | 555 | | | | | 560 |
| | Ala | Gly | Thr | Asp | Pro | Asn | Met | Ala | Asp | Asn | Gly | Asp | Leu | Asp | Leu | Gly |
| | | | | | 565 | | | | | 570 | | | | | 575 | |
| 40 | Pro | Val | Glu | Thr | Glu | Pro | Pro | Tyr | Ala | Ser | Pro | Arg | Tyr | Leu | Arg | Asn |
| | | | | 580 | | | | | 585 | | | | | 590 | | |
| | Phe | Thr | Leu | Thr | Val | Thr | Asp | Phe | Tyr | Arg | Ser | Trp | Asn | Cys | Ala | Pro |
| 45 | | | 595 | | | | | 600 | | | | | 605 | | | |
| | Gly | Pro | Phe | His | Leu | Phe | Pro | His | Thr | Pro | Phe | Asp | Pro | Val | Leu | Pro |
| | | 610 | | | | | 615 | | | | | 620 | | | | |
| | Ser | Glu | Ala | Lys | Phe | Leu | Gly | Ser | Gly | Thr | Gly | Phe | Arg | Pro | Ile | Gly |
| 50 | 625 | | | | | 630 | | | | | 635 | | | | | 640 |
| | Gly | Gly | Ala | Gly | Gly | Ser | Gly | Lys | Glu | Phe | Gln | Ala | Ala | Leu | Gly | Gly |
| | | | | | 645 | | | | | 650 | | | | | 655 | |
| 55 | Asn | Val | Pro | Arg | Glu | Gln | Phe | Thr | Val | Val | Met | Leu | Thr | Tyr | Glu | Arg |
| | | | | 660 | | | | | 665 | | | | | 670 | | |
| | Glu | Glu | Val | Leu | Met | Asn | Ser | Leu | Glu | Arg | Leu | Asn | Gly | Leu | Pro | Tyr |
| 60 | | | 675 | | | | | 680 | | | | | 685 | | | |
| | Leu | Asn | Lys | Val | Val | Val | Val | Trp | Asn | Ser | Pro | Lys | Leu | Pro | | |

(2) INFORMATION FOR SEQ ID NO:5:

50 (ii) MOLECULE TYPE: protein

60 Leu Cys Gly Glu Arg Glu Asp Arg Leu Glu Leu Lys Leu Ser Thr
 1 5 10 15

 Phe Ala Leu Ile Ile Thr Pro Gly Asp Pro Arg Leu Val Ile Ser Ser
 20 25 30

Gly Cys Ala Thr Arg Leu Phe Glu Ala Leu Glu Val Gly Ala Val Pro
 35 40 45
 Val Val Leu Gly Glu Gln Val Gln Leu Pro Tyr Gln Asp Met Leu Gln
 5 50 55 60
 Trp Asn Glu Ala Ala Leu Val Val Pro Lys Pro Arg Val Thr Glu Val
 65 70 75 80
 His Phe Leu Leu Arg Ser Leu Ser Asp Ser Asp Leu Leu Ala Met Arg
 10 85 90 95
 Arg Gln Gly Arg Phe Leu Trp Glu Thr Tyr Phe Pro Thr Ala Asp Ser
 100 105 110
 Ile Phe Asn Thr Val Leu Ala Met Ile Arg Thr Arg Ile
 15 115 120 125

(2) INFORMATION FOR SEQ ID NO:6:

20 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 120 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 25 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Arg Cys His Lys His Gln Val Phe Asp Tyr Pro Gln Val Leu Gln Glu
 35 1 5 10 15
 Ala Thr Phe Cys Val Val Leu Arg Gly Ala Arg Leu Gly Gln Ala Val
 20 25 30
 Leu Ser Asp Val Leu Gln Ala Gly Cys Val Pro Val Val Ile Ala Asp
 40 35 40 45
 Ser Tyr Ile Leu Pro Phe Ser Glu Val Leu Asp Trp Lys Arg Ala Ser
 50 55 60
 Val Val Val Pro Glu Glu Lys Met Ser Asp Val Tyr Ser Ile Leu Gln
 45 65 70 75 80
 Ser Ile Pro Gln Arg Gln Ile Glu Glu Met Gln Arg Gln Ala Arg Trp
 50 85 90 95
 Phe Trp Glu Ala Tyr Phe Gln Ser Ile Lys Ala Ile Ala Leu Ala Thr
 100 105 110
 Leu Gln Ile Ile Asn Asp Arg Ile
 55 115 120

(2) INFORMATION FOR SEQ ID NO:7:

60 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

10 Arg Cys Asp Arg Asp Asn Thr Glu Tyr Glu Lys Tyr Asp Tyr Arg Glu
1 5 10 15

Met Leu His Asn Ala Thr Phe Cys Leu Val Pro Arg Gly Arg Arg Leu
20 25 30

15 Gly Ser Phe Arg Phe Leu Glu Ala Leu Gln Ala Ala Cys Val Pro Val
35 40 45

20 Met Leu Ser Asn Gly Trp Glu Leu Pro Phe Ser Glu Val Ile Asn Trp
50 55 60

Asn Gln Ala Ala Val Ile Gly Asp Glu Arg Leu Leu Leu Gln Ile Pro
65 70 75 80

25 Ser Thr Ile Arg Ser Ile His Gln Asp Lys Ile Leu Ala Leu Arg Gln
85 90 95

Gln Thr Gln Phe Leu Trp Glu Ala Tyr Phe Ser Ser Val Glu Lys Ile
100 105 110

30 Val Leu Thr Thr Leu Glu Ile Ile Gln Asp Arg Ile
115 120

(2) INFORMATION FOR SEQ ID NO:8:

35

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

50 Arg Cys Glu Gln Asp Pro Gly Pro Gly Gln Thr Gln Arg Gln Glu Thr
1 5 10 15

Leu Pro Asn Ala Thr Phe Cys Leu Ile Ser Gly His Arg Pro Glu Ala
20 25 30

55 Ala Ser Arg Phe Leu Gln Ala Leu Gln Ala Gly Cys Ile Pro Val Leu
35 40 45

Leu Ser Pro Arg Trp Glu Leu Pro Phe Ser Glu Val Ile Asp Trp Thr
50 55 60

60 Lys Ala Ala Ile Val Ala Asp Glu Arg Leu Pro Leu Gln Val Leu Ala
65 70 75 80

TOPIC: 031601

Thr Gln Phe Leu Trp Asp Ala Tyr Phe Ser Ser Val Glu Lys Val Ile
100 105 110

10(2) INFORMATION FOR SEQ ID NO:9:

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Gly Ser Ser Thr Phe Cys Phe Leu Leu Pro Ser Glu Met Phe Phe Gln
20 25 30

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Gln Ser Phe Glu Ile Ser Asp Ile Ile Glu Met Arg Arg Val Gly Arg
85 90 95

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(2) INFORMATION FOR SEQ ID NO:10:

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Val Pro Arg Glu Gln Phe Thr Val Val Met Leu Thr Tyr Glu Arg Glu
 1 5 10 15
 Glu Val Leu Met Asn Ser Leu Glu Arg Leu Asn Gly Leu Pro Tyr Leu
 5 20 25 30
 Asn Lys Val Val Val Val Trp Asn Ser Pro Lys Leu Pro Ser Glu Asp
 35 40 45
 Leu Leu Trp Pro Asp Ile Gly Val Pro Ile Met Val Val Arg Thr Glu
 10 50 55 60
 Lys Asn Ser Leu Asn Asn Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr
 15 65 70 75 80
 Glu Ala Ile Leu Ser Ile Asp Asp Asp Ala His Leu Arg His Asp Glu
 85 90 95
 Ile Met Phe Gly Phe Arg Val Trp Arg Glu Ala Arg Asp Arg Ile Val
 20 100 105 110
 Gly Phe Pro Gly Arg Tyr His Ala Trp Asp Ile Pro His Gln Ser Trp
 115 120 125
 Leu Tyr Asn Ser Asn Tyr Ser Cys Glu Leu Ser Met Val Leu Thr Gly
 25 130 135 140
 Ala Ala Phe Phe His Lys Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met
 145 150 155 160
 Pro Gln Ala Ile Arg Asp Met Val Asp Glu Tyr Ile Asn Cys Glu Asp
 165 170 175
 Ile Ala Met Asn Phe Leu Val Ser His Ile Thr Arg Lys Pro Pro Ile
 35 180 185 190
 Lys Val Thr Ser Arg Trp Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala
 195 200 205
 Leu Ser His Asp Asp Ser His Phe His Glu Arg His Lys Cys Ile Asn
 40 210 215 220
 Phe Phe Val Lys Val Tyr Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe
 225 230 235 240
 Arg Val Asp Ser Val Leu Phe Lys Thr Arg Leu Pro His Asp Lys Thr
 245 250 255
 Lys Cys Phe Lys Phe Ile
 50 260

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 55 (A) LENGTH: 269 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 60 (ii) MOLECULE TYPE: protein

FOOTED-02660860

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

5 Pro Gln Ser Gln Gly Phe Thr Gln Ile Val Leu Thr Tyr Asp Arg Val
 1 5 10 15
 Glu Ser Leu Phe Arg Val Ile Thr Glu Val Ser Lys Val Pro Ser Leu
 20 25 30
 10 Ser Lys Leu Leu Val Val Trp Asn Asn Gln Asn Lys Asn Pro Pro Glu
 35 40 45
 Asp Ser Leu Trp Pro Lys Ile Arg Val Pro Leu Lys Val Val Arg Thr
 50 55 60
 15 Ala Glu Asn Lys Leu Ser Asn Arg Phe Phe Pro Tyr Asp Glu Ile Glu
 65 70 75 80
 Thr Glu Ala Val Leu Ala Ile Asp Asp Asp Ile Ile Met Leu Thr Ser
 85 90 95
 20 Asp Glu Leu Gln Phe Gly Tyr Glu Val Trp Arg Glu Phe Pro Asp Arg
 100 105 110
 Leu Val Gly Tyr Pro Gly Arg Leu His Leu Trp Asp His Glu Ala Met
 115 120 125
 25 Asn Lys Trp Lys Tyr Glu Ser Glu Trp Thr Asn Glu Val Ser Met Val
 130 135 140
 30 Leu Thr Gly Ala Ala Phe Tyr His Lys Tyr Phe Asn Tyr Leu Tyr Thr
 145 150 155 160
 Lys Met Pro Gly Asp Ile Lys Asn Trp Val Asp Ala His Met Asn Cys
 165 170 175
 35 Tyr Glu Asp Ile Ala Met Asn Phe Leu Val Ala Asn Val Thr Gly Lys
 180 185 190
 40 Ala Val Ile Lys Val Thr Pro Arg Lys Lys Phe Lys Cys Pro Glu Cys
 195 200 205
 Thr Ala Ile Asp Gly Leu Ser Leu Asp Gln Thr His Met Val Glu Arg
 210 215 220
 45 Ser Glu Cys Ile Asn Lys Phe Ala Ser Val Phe Gly Thr Met Pro Leu
 225 230 235 240
 Lys Val Val Glu His Arg Ala Asp Pro Val Leu Tyr Lys Asp Asp Phe
 245 250 255
 50 Pro Glu Lys Leu Lys Ser Phe Pro Asn Ile Gly Ser Leu
 260 265

(2) INFORMATION FOR SEQ ID NO:12:

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(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

60

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

5 Pro Pro Ser Lys Phe Thr Ala Val Ile His Ala Val Thr Pro Leu Val
 1 5 10 15

 Ser Gln Ser Gln Pro Val Leu Lys Leu Leu Val Ala Ala Ala Lys Ser
 20 25 30

10 Gln Tyr Cys Ala Gln Ile Ile Val Leu Trp Asn Cys Asp Lys Pro Leu
 35 40 45

15 Pro Ala Lys His Arg Trp Pro Ala Thr Ala Val Pro Val Val Val Ile
 50 55 60

 Glu Gly Glu Ser Lys Val Met Ser Ser Arg Phe Leu Pro Tyr Asp Asn
 65 70 75 80

20 Ile Ile Thr Asp Ala Val Leu Ser Leu Asp Glu Asp Thr Val Leu Ser
 85 90 95

 Thr Thr Glu Val Asp Phe Ala Phe Thr Val Trp Gln Ser Phe Pro Glu
 100 105 110

25 Arg Ile Val Gly Tyr Pro Ala Arg Ser His Phe Trp Asp Asn Ser Lys
 115 120 125

30 Glu Arg Trp Gly Tyr Thr Ser Lys Trp Thr Asn Asp Tyr Ser Met Val
 130 135 140

 Leu Thr Gly Ala Ala Ile Tyr His Lys Tyr Tyr His Tyr Leu Tyr Ser
 145 150 155 160

35 His Tyr Leu Pro Ala Ser Leu Lys Asn Met Val Asp Gln Leu Ala Asn
 165 170 175

 Cys Glu Asp Ile Leu Met Asn Phe Leu Val Ser Ala Val Thr Lys Leu
 180 185 190

40 Pro Pro Ile Lys Val Thr Gln Lys Lys Gln Tyr Lys Glu Thr Met Met
 195 200 205

45 Gly Gln Thr Ser Arg Ala Ser Arg Trp Ala Asp Pro Asp His Phe Ala
 210 215 220

 Gln Arg Gln Ser Cys Met Asn Thr Phe Ala Ser Trp Phe Gly Tyr Met
 225 230 235 240

50 Pro Leu Ile His Ser Gln Met Arg Leu Asp Pro Val Leu Lys Asp Gln
 245 250 255

 Val Ser Ile Leu Arg Lys Lys Tyr Arg Asp Ile Glu Arg Leu
 260 265 270

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(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- 60 (A) LENGTH: 262 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

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Arg Thr Leu Ala Asp Glu Ala Pro Thr Cys Val Asp Val Leu Met Asn
165 170 175

Gly Lys Gln Arg Gln Glu Ala Ala Pro Leu Ala Pro Gly Gly Pro Gly
195 200 205

Pro Arg Pro Lys Pro Pro Ala Pro Ala Pro Asp Cys Ile Asn Gln Ile
210 215 220

Ala Ala Ala Phe Gly His Met Pro Leu Leu Ser Ser Arg Leu Arg Leu
225 230 235 240

Asp Pro Val Leu Phe Lys Asp Pro Val Ser Val Gln Arg Lys Lys Tyr
245 250 255

Arg Ser Leu Glu Lys Pro
260

(2) INFORMATION FOR SEQ ID NO:14:

60

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 270 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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Ser Thr Met Asp Ser Phe Thr Leu Ile Met Gln Thr Tyr Asn Arg Thr
1 5 10 15

15

Asp Leu Leu Leu Lys Leu Leu Asn His Tyr Gln Ala Val Pro Asn Leu
20 25 30

His Lys Val Ile Val Val Trp Asn Asn Ile Gly Glu Lys Ala Pro Asp
35 40 45

20

Glu Leu Trp Asn Ser Leu Gly Pro His Pro Ile Pro Val Ile Phe Lys
50 55 60

Gln Gln Thr Ala Asn Arg Met Arg Asn Arg Leu Gln Val Phe Pro Glu
65 70 75 80

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Leu Glu Thr Asn Ala Val Leu Met Val Asp Asp Asp Thr Leu Ile Ser
85 90 95

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Thr Pro Asp Leu Val Phe Ala Phe Ser Val Trp Gln Gln Phe Pro Asp
100 105 110

Gln Ile Val Gly Phe Val Pro Arg Lys His Val Ser Thr Ser Ser Gly
115 120 125

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Ile Tyr Ser Tyr Gly Ser Phe Glu Met Gln Ala Pro Gly Ser Gly Asn
130 135 140

Gly Asp Gln Tyr Ser Met Val Leu Ile Gly Ala Ser Phe Phe Asn Ser
145 150 155 160

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Lys Tyr Leu Glu Leu Phe Gln Arg Gln Pro Ala Ala Val His Ala Leu
165 170 175

Ile Asp Asp Thr Gln Asn Cys Asp Asp Ile Ala Met Asn Phe Ile Ile
180 185 190

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Ala Lys His Ile Gly Lys Thr Ser Gly Ile Phe Val Lys Pro Val Asn
195 200 205

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Met Asp Asn Leu Glu Lys Glu Thr Asn Ser Gly Tyr Ser Gly Met Trp
210 215 220

His Arg Ala Glu His Ala Leu Gln Arg Ser Tyr Cys Ile Asn Lys Leu
225 230 235 240

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Val Asn Ile Tyr Asp Ser Met Pro Leu Arg Tyr Ser Asn Ile Met Ile
245 250 255

60

Ser Gln Phe Gly Phe Pro Tyr Ala Asn Tyr Lys Arg Lys Ile
260 265 270

(2) INFORMATION FOR SEQ ID NO:15:

09809920-031601

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

15 Arg Gln Arg Glu Gln Phe Thr Val Val Leu Leu Thr Tyr Glu Arg Asp
 1 5 10 15
 Ala Val Leu Thr Gly Ala Leu Glu Arg Leu His Gln Leu Pro Tyr Leu
 20 20 25 30
 Asn Lys Ile Ile Val Val Trp Asn Asn Val Asn Arg Asp Pro Pro Asp
 35 40 45
 Ser Trp Pro Ser Leu His Ile Pro Val Glu Phe Ile Arg Val Ala Glu
 50 55 60
 25 Asn Asn Leu Asn Asn Arg Phe Val Pro Trp Asp Arg Ile Glu Thr Glu
 65 70 75 80
 Ala Val Leu Ser Leu Asp Asp Asp Ile Asp Leu Met Gln Gln Glu Ile
 85 90 95
 30 Ile Leu Ala Phe Arg Val Trp Arg Glu Asn Arg Asp Arg Ile Val Gly
 100 105 110
 Phe Pro Ala Arg His His Ala Arg Tyr Gly Asp Ser Met Phe Tyr Asn
 115 120 125
 Ser Asn His Thr Cys Gln Met Ser Met Ile Leu Thr Gly Ala Ala Phe
 130 135 140
 40 Ile His Lys Asn Tyr Leu Thr Ala Tyr Thr Tyr Glu Met Pro Ala Glu
 145 150 155 160
 Ile Arg Glu His Val Asn Ser Ile Lys Asn Cys Glu Asp Ile Ala Met
 165 170 175
 45 Asn Tyr Leu Val Ser His Leu Thr Arg Lys Pro Pro Ile Lys Thr Thr
 180 185 190
 Ser Arg Trp Thr Leu Lys Cys Pro Thr Cys Thr Glu Ser Leu Tyr Lys
 195 200 205
 Glu Gly Thr His Phe Glu Lys Arg His Glu Cys Met Arg Leu Phe Thr
 210 215 220
 55 Lys Ile Tyr Gly Tyr Asn Pro Leu Lys Phe Ser Gln Phe Arg Ala Asp
 225 230 235 240
 Ser Ile Leu Phe Lys Thr Arg Leu Pro Gln Asn His Gln Lys Cys Phe
 245 250 255
 60 Lys Tyr Val

TOPREF 02660350

(2) INFORMATION FOR SEQ ID NO:16:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTATGGCGAG TGACCCGACG TG

22

20 (2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

35TTGCTAAAGT GAAGGAAGTT GG

22

(2) INFORMATION FOR SEQ ID NO:18:

- 40 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

45 (ii) MOLECULE TYPE: DNA (genomic)

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACCCGACGTG ATCTGG

16

(2) INFORMATION FOR SEQ ID NO:19:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

5AAGAGCTCCT GCAGCTGG

18

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTCTCGTTGC CCTCTCAC

18

(2) INFORMATION FOR SEQ ID NO:21:

25

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCATCAATC TGTCACG

17

40

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

55

ACTACGATGA CCGGATC

17

(2) INFORMATION FOR SEQ ID NO:23:

60

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

18

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

16

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

40

TATTGGTGGT GGAGCTGG

18

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AATCCAGCCA TGGTCTCCTT GG

22

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

5

(ii) MOLECULE TYPE: DNA (genomic)

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AGTCGATGCC ATTATTACCA GC

22

15

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

20

(ii) MOLECULE TYPE: DNA (genomic)

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

30

TTCCTTCCTC ATCACAG

17

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

35

40

(ii) MOLECULE TYPE: DNA (genomic)

45

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGGTCTGTGT ATGCACTTGT G

21

50 (2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55

(ii) MOLECULE TYPE: DNA (genomic)

60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

09809920-031601

AGTCGATGCC ATTATTACCA GC

22

(2) INFORMATION FOR SEQ ID NO:31:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 10 (ii) MOLECULE TYPE: DNA (genomic)

- 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTCAAGGGTG TGGAGAG

17

20 (2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

30

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

35 TTGGCTGAAA GCCAACAACC TG

22

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 40 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- 45 (ii) MOLECULE TYPE: DNA (genomic)

- 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

AACATGCACG CATCCACAGC

20

(2) INFORMATION FOR SEQ ID NO:34:

- 55 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 60 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

5TTGTAACACA GCATGTGG

18

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: DNA (genomic)

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGTTCTGTCA GTATTAGCTG GG

22

(2) INFORMATION FOR SEQ ID NO:36:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
30 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

TTCCTCCCTC TGCTCATCCT C

21

40

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
45 (B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

55 TTCCCACTCT GTCTCTC

17

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